

SEQUENCE LISTING

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<120> NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES IN PATHOGENIC
MYCOBACTERIA AND THEIR USE AS DIAGNOSTICS, VACCINES AND
TARGETS FOR CHEMOTHERAPY

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<140> 09/091,538

<141> 1998-06-19

<150> PCT/GB96/03221

<151> 1996-12-23

<150> GB 9526178.0

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 catcgcaaac agtttccgcc cggaactcgg ctgcgactg gtcgttcaca gcgggcccga 3540

00705911-10660

tgatggccacacgacgcca tgaaccgcgg cgctcggcgta gccacagcg aatgggtact 3600
 ttttttaggc gccgacgaca ccctctacga accaaccacg ttggcccagg tagccgcttt 3660
 tctcggcgac catgcggcaa gccatcttgt ctatggcgat gttgtgatgc gttcgacgaa 3720
 aagccggcat gccggacctt tcgacctcga ccgcctccta tttgagacga atttgtgcca 3780
 ccaatcgatc ttttaccgcc gtgagctttt cgacggcatc ggcccttaca acctgcgcta 3840
 ccgagtctgg gcggaactggg acttcaatat tcgctgcttc tccaaccgg cgctgattac 3900
 ccgctacatg gacgtcgtga tttccgaata caacgacatg accggcttca gcatgaggca 3960
 ggggactgat aaagagttca gaaaacggct gccaatgtac ttctgggttg caggggtggga 4020
 gacttgcagg cgcatgctgg cgtttttgaa agacaaggag aatcgccgtc tggccttgcg 4080
 tacgcggttg ataagggtta aggccgtctc caaagaacga agcgcagaac cgtagtcgcg 4140
 gatccacatt ggacttcttt aacgcgtttg cgtcctgac cactttcaa ccccgttccg 4200
 cgtgacgcgg cgcgagaga gtggtcgcat atcgcgtcac tgttctcgtg ccagtgttg 4260
 gaaagcgteg agcactctgg ttcgcgttct tgacgttcgc gcccgccct agaggtagcg 4320
 tgtcacgtga ctgaagccaa tgagtgaac tcggcgtcgc gaaaggtttc agtcgcgggtt 4380
 gagcaagaca ccgcaagact actggagtgc gtgcacaagc gcctccagct cacgg 4435

<210> 5
 <211> 378
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(375)

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 Met Ile Ala Val Ile Trp Ser Ala Val Pro Thr Gly Thr Val Asp Leu
 1 5 10 15
 tgc acg atc acc ttg tac cgg tgc atg tat gac cca atg tgc tcc gca 96
 Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala
 20 25 30
 acc gag aag acg tac gtc agg tcc gcc gcc ccg ctt tca ccc atg ggc 144
 Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly
 35 40 45
 gtc ggg acg gcg atg aaa atg acg tcc gcg tgc tgc att ccg cgt tgc 192
 Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys
 50 55 60
 cgg tgc gtg gtg aag tca atc agc ccg ttc tca cgg ttc ctc gca atc 240
 Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile
 65 70 75 80

0070594-140500

aac tcc caa ccc ggg ctc gaa aat cgg gac act gcc tgc gag gag caa 288
 Asn Ser Gln Pro Gly Leu Glu Asn Arg Asp Thr Ala Cys Glu Glu Gln
 85 90 95

atc gat ctt ggc ctg atc gat atc gac aca gac gac atc gtt gcc gct 336
 Ile Asp Leu Gly Leu Ile Asp Ile Asp Thr Asp Asp Ile Val Ala Ala
 100 105 110

atc cgc gag aca ggc gcc cgt gac gag gcc tac ata gcc tga 378
 Ile Arg Glu Thr Gly Ala Arg Asp Glu Ala Tyr Ile Ala
 115 120 125

<210> 6
 <211> 125
 <212> PRT
 <213> Mycobacterium

<400> 6
 Met Ile Ala Val Ile Trp Ser Ala Val Pro Thr Gly Thr Val Asp Leu
 1 5 10 15

Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala
 20 25 30

Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly
 35 40 45

Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys
 50 55 60

Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile
 65 70 75 80

Asn Ser Gln Pro Gly Leu Glu Asn Arg Asp Thr Ala Cys Glu Glu Gln
 85 90 95

Ile Asp Leu Gly Leu Ile Asp Ile Asp Thr Asp Asp Ile Val Ala Ala
 100 105 110

Ile Arg Glu Thr Gly Ala Arg Asp Glu Ala Tyr Ile Ala
 115 120 125

<210> 7
 <211> 834
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(831)

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 Val Ser Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Leu Asn Asp
 1 5 10 15

ctc gag	atg aaa agc acc gtg gag agc gtt cgc	cag cgc tat	96
Leu Glu	Leu Lys Ser Thr Val Glu Ser Val Arg	Gln Arg Tyr	
	20	25 30	
ggg ggg cga atc gag cac atc gtc atc gac ggt gga tcg ggc gac gcc			144
Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala			
	35 40	45	
gtc gtg gag tat ctg tcc ggc gat cct ggc ttt gca tat tgg caa tct			192
Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser			
	50 55	60	
cag ccc gac aac ggg aga tat gac gcg atg aat cag ggc att gcc cat			240
Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His			
	65 70	75 80	
tcg tcg ggc gac ctg ttg tgg ttt atg cac tcc acg gat cgt ttc tcc			288
Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser			
	85 90	95	
gat cca gat gca gtc gct tcc gtg gtg gag gcg ctc tcg ggg cat gga			336
Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly			
	100 105	110	
cca gta cgt gat ttg tgg ggt tac ggg aaa aac aac ctt gtc gga ctc			384
Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu			
	115 120	125	
gac ggc aaa cca ctt ttc cct cgg ccg tac ggc tat atg ccg ttt aag			432
Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys			
	130 135	140	
atg cgg aaa ttt ctg ctc ggc gcg acg gtt gcg cat cag gcg aca ttc			480
Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe			
	145 150	155 160	
ttc ggc gcg tcg ctg gta gcc aag ttg ggc ggt tac gat ctt gat ttt			528
Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe			
	165 170	175	
gga ctc gag gcg gac cag ctg ttc atc tac cgt gcc gca cta ata cgg			576
Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg			
	180 185	190	
cct ccc gtc acg atc gac cgc gtg gtt tgc gac ttc gat gtc acg gga			624
Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly			
	195 200	205	
cct ggt tca acc cag ccc atc cgt gag cac tat cgg acc ctg cgg cgg			672
Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg			
	210 215	220	
ctc tgg gac ctg cat ggc gac tac ccg ctg ggt ggg cgc aga gtg tcg			720
Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser			
	225 230	235 240	
tgg gct tac ttg cgt gtg aag gag tac ttg att cgg gcc gac ctg gcc			768
Trp Ala Tyr Leu Arg Val Lys Glu Tyr Leu Ile Arg Ala Asp Leu Ala			
	245 250	255	

00905011-110600

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<400> 8
Val Ser Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Leu Asn Asp
  1          5          10          15
Leu Glu Gly Leu Lys Ser Thr Val Glu Ser Val Arg Ala Gln Arg Tyr
  20          25          30
Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala
  35          40          45
Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser
  50          55          60
Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His
  65          70          75          80
Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser
  85          90          95
Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly
 100          105          110
Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu
 115          120          125
Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys
 130          135          140
Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe
 145          150          155          160
Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe
 165          170          175
Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg
 180          185          190
Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly
 195          200          205
Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg
 210          215          220
Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser
 225          230          235          240

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Trp Ala T Leu Arg Val Lys Glu Tyr Leu Ile Arg Asp Leu Ala
 245 250 255

Ala Phe Asn Ala Val Lys Phe Leu Arg Ala Lys Phe Ala Arg Ala Ser
 260 265 270

Arg Lys Gln Asn Ser
 275

<210> 9
 <211> 1032
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1029)

<400> 9
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 Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
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 ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt 96
 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
 20 25 30
 cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt 144
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc 192
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat 240
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac 288
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt 336
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct 384
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg 432
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser
 130 135 140
 acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg 480
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160

tac tgg aac tgc cgc aac tat cga gag gcg tac gga ttc gca gtg 528
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175

aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc 576
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190

gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc 624
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val
 195 200 205

caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc 672
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly
 210 215 220

tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct 720
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro
 225 230 235 240

gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt 768
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg
 245 250 255

gag ttc gct caa gct gct ttt gac cat gtc ggg ctc gac tgg caa aag 816
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys
 260 265 270

cgc gtc aag ttt gac gac cgc tat ttg cgt ccc acc gag gtc gat tcg 864
 Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285

cta gta gga gat gcc gac aag gcg gcc cag tca ctc ggc tgg aaa gct 912
 Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala
 290 295 300

tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc 960
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile
 305 310 315 320

gcc gcg ttg gag tgc gat ggc aca cca tgg atc gac acg ccg atg ttg 1008
 Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu
 325 330 335

cct ggt tgg ggc aga gta agt tga 1032
 Pro Gly Trp Gly Arg Val Ser
 340

<210> 10
 <211> 343
 <212> PRT
 <213> Mycobacterium

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 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
 20 25 30

Arg Arg Ala Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser
 130 135 140
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val
 195 200 205
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly
 210 215 220
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro
 225 230 235 240
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg
 245 250 255
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys
 260 265 270
 Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala
 290 295 300
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile
 305 310 315 320
 Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu
 325 330 335
 Pro Gly Trp Gly Arg Val Ser
 340

<210> 11
 <211> 103
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1029)

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 Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
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 ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt 96
 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
 20 25 30
 cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt 144
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc 192
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat 240
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac 288
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt 336
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct 384
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg 432
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Gln Asn Glu Ser
 130 135 140
 acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg 480
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160
 tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg 528
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc 576
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc 624
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val
 195 200 205

caa tgc gac tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc 672
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly
 210 215 220
 tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct 720
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro
 225 230 235 240
 gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt 768
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg
 245 250 255
 gag ttc gct caa gct gct ttt gac cac gtc ggg ctc gac tgg caa aag 816
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys
 260 265 270
 cac gtc aag ttt gac gac cgc tat ttg cgc ccc acc gag gtc gat tgc 864
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 cta gta gga gat gcc gac agg gcg gcc cag tca ctc ggc tgg aaa gct 912
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala
 290 295 300
 tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc 960
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile
 305 310 315 320
 gcc gcg tcg gag tgc gat ggc aca cca tgg atc gac acg ccg atg ttg 1008
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu
 325 330 335
 cct ggt tgg ggc gga gta agt tga 1032
 Pro Gly Trp Gly Gly Val Ser
 340

<210> 12
 <211> 343
 <212> PRT
 <213> Mycobacterium

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 20 25 30
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95

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cag agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro	96																		
20 25 30																			
gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg	144																		
35 40 45																			
aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	192																		
50 55 60																			
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	240																		
65 70 75 80																			
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile	288																		
85 90 95																			
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	336																		
100 105 110																			
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	384																		
115 120 125																			
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	432																		
130 135 140																			
cct atc cac gag agt gct tta ttg act ggc cct ttg gag ccc acc aac Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	480																		
145 150 155 160																			
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	528																		
165 170 175																			
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	576																		
180 185 190																			
ctc tac gga ccc ggc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	624																		
195 200 205																			
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	672																		
210 215 220																			
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	720																		
225 230 235 240																			

gtc gac gac ggc ggc agc gca tgc ctg ttc ctt ttg tat ttc gat 768
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp 255
 245 250

ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc 816
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser 270
 260 265

gag atc gca gac atg gtc gct aca ggc gtg ggc tac atc ggc gaa aca 864
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr 285
 275 280

cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp 300
 290 295

gtc tcc ggc cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys 320
 305 310 315

gac ggc atc gat gca acg gtg tgc tgg tac cgc aca aat gcc gat gcc 1008
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala 335
 325 330

gtg agg agg taa 1020
 Val Arg Arg

<210> 14
 <211> 339
 <212> PRT
 <213> Mycobacterium

<400> 14
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Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro 30
 20 25

Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg 45
 35 40

Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp 60
 50 55

Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu 80
 65 70 75

Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile 95
 85 90

Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg 110
 100 105

Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg 125
 115 120

Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln 140
 130 135

Pro Ile His Ser Ala Leu Leu Thr Gly Pro Leu Gln Thr Asn
 145 150 155 160
 Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala
 165 170 175
 Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn
 180 185 190
 Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu
 195 200 205
 Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu
 210 215 220
 Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His
 225 230 235 240
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp
 245 250 255
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser
 260 265 270
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr
 275 280 285
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp
 290 295 300
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys
 305 310 315 320
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala
 325 330 335
 Val Arg Arg

<210> 15
 <211> 1020
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1017)

<400> 15
 gtg cga tgg cac acc atg gat cga cac gcc gat gtt gcc tgg ttg ggg 48
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly
 1 5 10 15
 cgg agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc 96
 Arg Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro
 20 25 30
 gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt 144
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg
 35 40 45

aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act ggc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc ggc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	
gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat	768
Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp	
245 250 255	
ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc	816
Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser	
260 265 270	
gag atc gca gac atg gtc gct acg gcg gtg ggc tac atc ggc gaa aca	864
Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr	
275 280 285	

cgt tgg gga cca act aaa ccc gat gga acc ccg cgc cta ttg gac 912
 Arg Trp Asn Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp
 290 295 300

gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys
 305 310 315 320

gac gcc atc gat gca acg gtg tcg tgg tac cgc aca aat gcc gat gcc 1008
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala
 325 330 335

gtg agg agg taa 1020
 Val Arg Arg

<210> 16
 <211> 339
 <212> PRT
 <213> Mycobacterium

<400> 16
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly
 1 5 10 15
 Arg Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro
 20 25 30
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg
 35 40 45
 Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp
 50 55 60
 Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu
 65 70 75 80
 Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile
 85 90 95
 Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg
 100 105 110
 Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg
 115 120 125
 Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln
 130 135 140
 Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn
 145 150 155 160
 Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala
 165 170 175
 Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn
 180 185 190
 Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu
 195 200 205

Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu
 210 215 220
 Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His
 225 230 235 240
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp
 245 250 255
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser
 260 265 270
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr
 275 280 285
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp
 290 295 300
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys
 305 310 315 320
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala
 325 330 335
 Val Arg Arg

 <210> 17
 <211> 723
 <212> DNA
 <213> Mycobacterium

 <220>
 <221> CDS
 <222> (1)..(720)

 <400> 17
 atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agt acc 48
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
 1 5 10 15
 gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96
 Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
 20 25 30
 aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc gcc 144
 Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
 35 40 45
 cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192
 Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
 50 55 60
 tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc aag tcg 240
 Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser
 65 70 75 80
 gca tcg gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
 85 90 95

00705041-110500

gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336
Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
100 105 110

tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384
Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
115 120 125

aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tcg gtt 432
Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
130 135 140

gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480
Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
145 150 155 160

gta cag ggt ttc gag aag cag gtt atc acg ggc agt aag tca acg ctt 528
Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu
165 170 175

aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576
Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
180 185 190

tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624
Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
195 200 205

cta ggt ttc aga ctg acg ggt ttg ttg ccc ggc ttt acg gat ccg cgc 672
Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
210 215 220

aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720
Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
225 230 235 240

tga 723

<210> 18
<211> 240
<212> PRT
<213> Mycobacterium

<400> 18
Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
1 5 10 15
Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
20 25 30
Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
35 40 45
Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
50 55 60
Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser
65 70 75 80

Ala Ser Asn Leu Trp Glu Cys His Gln Tyr Ala Ile Gly Asp Ala
85 90 95

Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
100 105 110

Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
115 120 125

Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
130 135 140

Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
145 150 155 160

Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu
165 170 175

Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
180 185 190

Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
195 200 205

Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
210 215 220

Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
225 230 235 240

<210> 19
<211> 723
<212> DNA
<213> Mycobacterium

<220>
<221> CDS
<222> (1)..(720)

<400> 19
atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agc acc 48
Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
1 5 10 15

gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96
Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
20 25 30

aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144
Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
35 40 45

cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192
Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
50 55 60

tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc gag tcg 240
Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser
65 70 75 80

0070561-10500

gca tcg gat cca cta tgg gag tgt cac cag tat gcc ctg ggc gac gcc 288
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
 85 90 95

gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
 100 105 110

tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
 115 120 125

aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tcg gtt 432
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
 130 135 140

gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
 145 150 155 160

gta cag ggt ttc gag aag cag gtt atc gcg ggc agt aag tca acg ctt 528
 Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu
 165 170 175

aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
 180 185 190

tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
 195 200 205

cta ggt ttc aga ctg acg ggt ttg ttg ccc gga ttt acg gat ccg cgc 672
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
 210 215 220

aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
 225 230 235 240

tga 723

<210> 20
 <211> 240
 <212> PRT
 <213> Mycobacterium

<400> 20
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
 1 5 10 15

Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
 20 25 30

Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
 35 40 45

Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
 50 55 60

Ser Phe G o Leu Ser Gly Pro Phe Ala Gln Leu rg Glu Ser
65 70 75 80

Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
85 90 95

Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
100 105 110

Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
115 120 125

Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
130 135 140

Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
145 150 155 160

Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu
165 170 175

Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
180 185 190

Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
195 200 205

Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
210 215 220

Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
225 230 235 240

<210> 21
<211> 801
<212> DNA
<213> Mycobacterium

<220>
<221> CDS
<222> (1)..(798)

<400> 21
atg act gcg cca gtg ttc tcg ata att atc cct acc ttc aat gca gcg 48
Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
1 5 10 15

gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg 96
Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg
20 25 30

gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc 144
Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu
35 40 45

gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt 192
Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val
50 55 60

cac agc ggc ggc gat gat ggc ccc tac gac gcc atg a gc ggc gtc 240
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val
 65 70 75 80

ggc gtg gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc 288
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr
 85 90 95

ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac 336
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp
 100 105 110

cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg 384
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr
 115 120 125

aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag 432
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu
 130 135 140

acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac 480
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp
 145 150 155 160

ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac 528
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp
 165 170 175

ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg 576
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met
 180 185 190

gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg 624
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg
 195 200 205

cag ggg act gat aaa gag ttc aga aaa cgg ctg cca atg tac ttc tgg 672
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp
 210 215 220

gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac 720
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp
 225 230 235 240

aag gag aat cgc cgt ctg gcc ttg cgt acg cgg ttg ata agg gtt aag 768
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys
 245 250 255

gcc gtc tcc aaa gaa cga agc gca gaa ccg tag 801
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 22
 <211> 266
 <212> PRT
 <213> Mycobacterium

<400> 22
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
 1 5 10 15

Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg
 20 25 30
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu
 35 40 45
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val
 50 55 60
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val
 65 70 75 80
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr
 85 90 95
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp
 100 105 110
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr
 115 120 125
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu
 130 135 140
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp
 145 150 155 160
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp
 165 170 175
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met
 180 185 190
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg
 195 200 205
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp
 210 215 220
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp
 225 230 235 240
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys
 245 250 255
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 23
 <211> 801
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(798)

00705944-10580

cca

[illegible]

aag gag a gc cgt ctg gcc ttg cgt acg cgg ttg agg gtt aag 768
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys
 245 250 255

gcc gtc tcc aaa gaa cga agc gca gaa ccg tag 801
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 24
 <211> 266
 <212> PRT
 <213> Mycobacterium

<400> 24
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
 1 5 10 15
 Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg
 20 25 30
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu
 35 40 45
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val
 50 55 60
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val
 65 70 75 80
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr
 85 90 95
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp
 100 105 110
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr
 115 120 125
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu
 130 135 140
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp
 145 150 155 160
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp
 165 170 175
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met
 180 185 190
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg
 195 200 205
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp
 210 215 220
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp
 225 230 235 240

0070504-140603

Lys Glu A Arg Arg Leu Ala Leu Arg Thr Arg Leu Arg Val Lys
 245 250 255

Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 25
 <211> 867
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(864)

<400> 25
 gtg gcc agc aga agt ccc cac tcc gct gcg ggt ggt tgg cta att ctt 48
 Val Ala Ser Arg Ser Pro His Ser Ala Ala Gly Gly Trp Leu Ile Leu
 1 5 10 15
 ggc ggc tcc ctt ctt gtg gtc ggc gtg gcg cat ccg gta gga ctc gcc 96
 Gly Gly Ser Leu Leu Val Val Gly Val Ala His Pro Val Gly Leu Ala
 20 25 30
 gga ggt gac gac gat gct ggc gtg gtg cag cag ccg atc gag gat gct 144
 Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala
 35 40 45
 ggc ggc ggt ggt gtg ctc ggg cag gaa tcg ccc cca ttg ttc gaa ggg 192
 Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly
 50 55 60
 cca atg cga ggc gat ggc cag gga gcg gcg ctc gta gcc ggc agc cac 240
 Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His
 65 70 75 80
 gag ccg gaa caa cag ttg agt ccc ggt gtc gtc gag ccg ggc gaa gcc 288
 Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala
 85 90 95
 gat ctc gtc caa gat gac cag atc cgc gcg gag cag ggt gtc gat gat 336
 Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp
 100 105 110
 ctt gcc gac ggt gtt gtc ggc cag gcc gcg gta gag gac ctc gat cag 384
 Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln
 115 120 125
 gtc ggc ggc ggt gaa gta gcg gac ttt gaa tcc ggc gtg gac ggc agc 432
 Val Gly Gly Gly Glu Val Ala Asp Phe Glu Ser Gly Val Asp Gly Ser
 130 135 140
 gtg ccc gca gcc gat gag cag gtg act ttt gcc cgt acc agg tgg gcc 480
 Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala
 145 150 155 160
 aat gac cgc cag gtt ctg ttg tgc ccg aat cca ttc cag gct cga cag 528
 Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln
 165 170 175

gta gtc gac ggt ggc tgc ggt gat cga cga tcc ggt gac gtc gaa ccc 576
 Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro
 180 185 190

gtc gag ggt ctt ggt gac cgg gaa ggc tgc ggc ctt gag acg gtt ggc 624
 Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly
 195 200 205

ggt gtt gga ggc atc gcg ggc agc gat ctc ggc ctc aac caa cgt ccg 672
 Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro
 210 215 220

cag gat ctc ctc cgg tgt cca gcg ttg cgt ctt ggc gac ttg caa cac 720
 Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His
 225 230 235 240

ctc ggc ggc gtt gcg gcg cac cgt ggc cag ctt caa ccg ccg cag cgc 768
 Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg
 245 250 255

cgc gtc aag gtc agc agc cag cgg tgc cgc cga gga cgg tgc cac cgg 816
 Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg
 260 265 270

ctt ggc agc ggt ggt cat gag gcc gtc ccg tcg gtg gtg ttg atc ttg 864
 Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu
 275 280 285

tag 867

<210> 26
 <211> 288
 <212> PRT
 <213> Mycobacterium

<400> 26
 Val Ala Ser Arg Ser Pro His Ser Ala Ala Gly Gly Trp Leu Ile Leu
 1 5 10 15

Gly Gly Ser Leu Leu Val Val Gly Val Ala His Pro Val Gly Leu Ala
 20 25 30

Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala
 35 40 45

Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly
 50 55 60

Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His
 65 70 75 80

Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala
 85 90 95

Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp
 100 105 110

Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln
 115 120 125

0070504140500

Val Gly G ly Glu Val Ala Asp Phe Glu Ser Gly Asp Gly Ser
 130 135 140

Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala
 145 150 155 160

Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln
 165 170 175

Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro
 180 185 190

Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly
 195 200 205

Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro
 210 215 220

Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His
 225 230 235 240

Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg
 245 250 255

Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg
 260 265 270

Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu
 275 280 285

<210> 27
 <211> 1739
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(945)

<400> 27
 atg ggc tgc ctc aaa ggt ggt gtc gtc gcc aat gtt gtt gtt cca aca 48
 Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val Val Pro Thr
 1 5 10 15

ccg gat tat gtg cga ttc gcg tcc cac tat ggc ttc gtt ccg gac ttc 96
 Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe
 20 25 30

tgc cac ggt gcg gat ccg caa tcg aag ggc atc gtg gag aac ctc tgt 144
 Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys
 35 40 45

ggc tac gct cag gac gac ctt gcg gtg ccg ctg ctg acc gaa gct gcg 192
 Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala
 50 55 60

tta gcc ggt gag cag gtc gac cta cgt gcc ctc aac gcc cag gcg caa 240
 Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln
 65 70 75 80

cta tgg tgc gag gtc aat gcc acg gtc cac tcg ggc tgc gcc 288
 Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala
 85 90 95

gtg ccc aac gat cgc ttg gtt gac gag cgc acc gtc ttg agg gag ctg 336
 Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu
 100 105 110

ccc tcg ctg cgg ccg acg atc ggc tcg ggg tcg gtg cgc cgt aag gtc 384
 Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val
 115 120 125

gac ggc ctc tcg tgc atc cgt tac ggc tca gct cgt tac tcg gtg cct 432
 Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro
 130 135 140

cag cgg ctc gtc ggt gcc acc gtg gcg gtg gtg gtc gat cat ggc gcc 480
 Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala
 145 150 155 160

ctg atc ctg ttg gaa cct gcg acc ggt gtg atc gtg gcc gag cac gag 528
 Leu Ile Leu Leu Glu Pro Ala Thr Gly Val Ile Val Ala Glu His Glu
 165 170 175

ctc gtc agc cca ggt gag gtg tcc atc ctc gat gaa cac tac gac gga 576
 Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly
 180 185 190

ccc aga ccc gca ccc tcg cgt ggt cct cgc ccg aaa acc caa gca gag 624
 Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu
 195 200 205

aaa cga ttc tgc gca ttg gga acc gaa gcg cag cag ttc ctc gtc ggt 672
 Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly
 210 215 220

gct gct gcg atc ggc aac acc cga ctg aaa tcc gaa ctc gac att ctg 720
 Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu
 225 230 235 240

ctc ggc ctt ggc gcc gcc cac ggc gaa cag gct ttg att gac gcg ctg 768
 Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu
 245 250 255

cgc cgg gcg gtt gcg ttt cgc cgg ttc cgc gct gcc gac gtg cgc tcg 816
 Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser
 260 265 270

atc ctg gcc gcc ggc gcc gcc acc cca caa ccc cgc ccc gcc gcc gac 864
 Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp
 275 280 285

gca ctc gtg ctc gat ctg ccc acc gtc gag acc cgc tcg ttg gag gcc 912
 Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala
 290 295 300

tac aag atc aac acc acc gac ggg acg gcc tca tgaccaccgc tgccaagccg 965
 Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser
 305 310 315

gtggcaccgt cctcggcggc accgctggct gctgaccttg acgcggcgct gcggcggttg 1025

aagctggcca cgggtgcgcc caacgccgcc gaggtgttgc aagtcgcca gacgcaacgc 1085
 tggacaccgg aggagatcct gcggacgttg gttgaggccg agatcgctgc ccgcgatgcc 1145
 tccaacaccg ccaaccgtct caaggccgca gccttcccgg tcaccaagac cctcgacggg 1205
 ttcgacgtca ccggatcgtc gatcaccgca gccacgttcg actacctgtc gagcctggaa 1265
 tggattcggg cacaacagaa cctggcggtc attggcccac ctggtacggg caaaagtcac 1325
 ctgctcatcg gctgcgggca cgctgccgtc cagccggat tcaaagtccg ctacttcacc 1385
 gccgccgacc tgatcgaggt cctctaccgc ggcttgccg acaacaccgt cggcaagatc 1445
 atcgacaccc tgctccgcgc ggatctggtc atcttgagc agatcggtt cgcctcgctc 1505
 gacgacaccg ggactcaact gttgttcgg ctcgtggctg ccggctacga gcgccgctcc 1565
 ctggccatcg cctcgattg gcccttcgaa caatgggggc gattcctgcc cgagcacacc 1625
 accgcgccca gcctcctga tcggctgctg caccacgcca gcctcgctg cacctccggc 1685
 gagtctacc ggatgcgcca cgcgcaccac aagaaggag ccgccaagaa ttag 1739

<210> 28
 <211> 315
 <212> PRT
 <213> Mycobacterium

<400> 28
 Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val Val Pro Thr
 1 5 10 15
 Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe
 20 25 30
 Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys
 35 40 45
 Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala
 50 55 60
 Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln
 65 70 75 80
 Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala
 85 90 95
 Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu
 100 105 110
 Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val
 115 120 125
 Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro
 130 135 140
 Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala
 145 150 155 160

Leu Ile Leu Glu Pro Ala Thr Gly Val Ile Val Ala Glu His Glu
 165 170 175
 Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly
 180 185 190
 Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu
 195 200 205
 Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly
 210 215 220
 Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu
 225 230 235 240
 Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu
 245 250 255
 Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser
 260 265 270
 Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp
 275 280 285
 Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala
 290 295 300
 Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser
 305 310 315

 <210> 29
 <211> 264
 <212> PRT
 <213> Mycobacterium

 <220>
 <221> DOMAIN
 <222> (1)..(264)
 <223> amino acid sequence is encoded by nucleotides
 945-1736 of SEQ ID NO:27

 <400> 29
 Met Thr Thr Ala Ala Lys Pro Val Ala Pro Ser Ser Ala Ala Pro Leu
 1 5 10 15
 Ala Ala Asp Leu Asp Ala Ala Leu Arg Arg Leu Lys Leu Ala Thr Val
 20 25 30
 Arg Arg Asn Ala Ala Glu Val Leu Gln Val Ala Lys Thr Gln Arg Trp
 35 40 45
 Thr Pro Glu Glu Ile Leu Arg Thr Leu Val Glu Ala Glu Ile Ala Ala
 50 55 60
 Arg Asp Ala Ser Asn Thr Ala Asn Arg Leu Lys Ala Ala Ala Phe Pro
 65 70 75 80
 Val Thr Lys Thr Leu Asp Gly Phe Asp Val Thr Gly Ser Ser Ile Thr
 85 90 95

Ala Ala Thr Phe Asp Tyr Leu Ser Ser Leu Glu Trp Ile Arg Ala Gln
 100 105 110

Gln Asn Leu Ala Val Ile Gly Pro Pro Gly Thr Gly Lys Ser His Leu
 115 120 125

Leu Ile Gly Cys Gly His Ala Ala Val His Ala Gly Phe Lys Val Arg
 130 135 140

Tyr Phe Thr Ala Ala Asp Leu Ile Glu Val Leu Tyr Arg Gly Leu Ala
 145 150 155 160

Asp Asn Thr Val Gly Lys Ile Ile Asp Thr Leu Leu Arg Ala Asp Leu
 165 170 175

Val Ile Leu Asp Glu Ile Gly Phe Ala Pro Leu Asp Asp Thr Gly Thr
 180 185 190

Gln Leu Leu Phe Arg Leu Val Ala Ala Gly Tyr Glu Arg Arg Ser Leu
 195 200 205

Ala Ile Ala Ser His Trp Pro Phe Glu Gln Trp Gly Arg Phe Leu Pro
 210 215 220

Glu His Thr Thr Ala Ala Ser Ile Leu Asp Arg Leu Leu His His Ala
 225 230 235 240

Ser Ile Val Val Thr Ser Gly Glu Ser Tyr Arg Met Arg His Ala Asp
 245 250 255

His Lys Lys Gly Ala Ala Lys Asn
 260

<210> 30
 <211> 789
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(786)

<400> 30
 gtg acg tct gct ccg acc gtc tcg gtg ata acg atc tcg ttc aac gac 48
 Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp
 1 5 10 15

ctc gac ggg ttg cag cgc acg gtg aaa agt gtg cgg gcg caa cgc tac 96
 Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr
 20 25 30

cgg gga cgc atc gag cac atc gta atc gac ggt ggc agc ggc gac gac 144
 Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp
 35 40 45

gtg gtg gca tac ctg tcc ggg tgt gaa cca ggc ttc gcg tat tgg cag 192
 Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln
 50 55 60

tcc gag c	ac ggc ggg cgg tac gac gcg atg aac	ggc atc gcg	240
Ser Glu P	Asp Gly Gly Arg Tyr Asp Ala Met Asn	Gly Ile Ala	
65	70	75	80
cac gca tcg ggt gat ctg ttg tgg ttc ttg cac tcc gcc gat cgt ttt	288		
His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe			
85	90	95	
tcc ggg ccc gac gtg gta gcc cag gcc gtg gag gcg cta tcc ggc aag	336		
Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys			
100	105	110	
gga ccg gtg tcc gaa ttg tgg ggc ttc ggg atg gat cgt ctc gtc ggg	384		
Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly			
115	120	125	
ctc gat cgg gtg cgc ggc ccg ata cct ttc agc ctg cgc aaa ttc ctg	432		
Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu			
130	135	140	
gcc ggc aag cag gtt gtt ccg cat caa gca tcg ttc ttc gga tca tcg	480		
Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser			
145	150	155	160
ctg gtg gcc aag atc ggt ggc tac gac ctt gat ttc ggg atc gcc gcc	528		
Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala			
165	170	175	
gac cag gaa ttc ata ttg cgg gcc gcg ctg gta tgc gag ccg gtc acg	576		
Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr			
180	185	190	
att ccg tgt gtg ctg tgc gag ttc gac acc acg ggc gtc ggc tcg cac	624		
Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His			
195	200	205	
ccg gaa cca agc gcg gtc ttc ggt gat ctg cgc cgc atg ggc gac ctt	672		
Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu			
210	215	220	
cat cgc cgc tac ccg ttc ggg gga agg cga ata tca cat gcc tac cta	720		
His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu			
225	230	235	240
cgc ggc cgg gag ttc tac gcc tac aac agt cga ttc tgg gaa aac gtc	768		
Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val			
245	250	255	
ttc acg cga atg tcg aaa tag	789		
Phe Thr Arg Met Ser Lys			
260			

<210> 31

<211> 262

<212> PRT

<213> Mycobacterium

<400> 31

Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp
1 5 10 15

Leu Asp Gly 20 Gln Arg Thr Val Lys Ser Val Arg Ala 30 Gln Arg Tyr
 Arg Gly Arg 35 Ile Glu His Ile Val 40 Ile Asp Gly Gly Ser 45 Gly Asp Asp
 Val Val Ala Tyr Leu Ser 55 Gly Cys Glu Pro Gly Phe 60 Ala Tyr Trp Gln
 Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala
 65 70 75 80
 His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe
 85 90 95
 Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys
 100 105 110
 Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly
 115 120 125
 Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu
 130 135 140
 Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser
 145 150 155 160
 Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala
 165 170 175
 Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr
 180 185 190
 Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His
 195 200 205
 Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu
 210 215 220
 His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu
 225 230 235 240
 Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val
 245 250 255
 Phe Thr Arg Met Ser Lys
 260

<210> 32
 <211> 1023
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1020)

<400> 32

gtg aag cga gcg ctc atc acc gga atc acc ggc cag gac ggc tcg tat	48
Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr	
1 5 10 15	
ctc gcc gaa ctg ctg ctg gcc aag ggg tat gag gtt cac ggg ctc atc	96
Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile	
20 25 30	
cgg cgc gct tcg acg ttc aac acc tcg cgg atc gat cac ctc tac gtc	144
Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val	
35 40 45	
gac ccg cac caa ccg ggc gcg cgg ctg ttt ctg cac tat ggt gac ctg	192
Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu	
50 55 60	
atc gac gga acc cgg ttg gtg acc ctg ctg agc acc atc gaa ccc gac	240
Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp	
65 70 75 80	
gag gtg tac aac ctg gcg gcg cag tca cac gtg cgg gtg agc ttc gac	288
Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp	
85 90 95	
gaa ccc gtg cac acc ggt gac acc acc ggc atg gga tcc atg cga ctg	336
Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu	
100 105 110	
ctg gaa gcc gtt cgg ctc tct cgg gtg cac tgc cgc ttc tat cag gcg	384
Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala	
115 120 125	
tcc tcg tcg gag atg ttc ggc gcc tcg ccg cca ccg cag aac gag ctg	432
Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu	
130 135 140	
acg ccg ttc tac ccg cgg tca ccg tat ggc gcc gcc aag gtc tat tcg	480
Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser	
145 150 155 160	
tac tgg gcg acc cgc aat tat cgc gaa gcg tac gga ttg ttc gcc gtt	528
Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val	
165 170 175	
aac ggc atc ttg ttc aat cac gaa tca ccg cgg cgc ggt gag acg ttc	576
Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe	
180 185 190	
gtg acc cga aag atc acc agg gcc gtg gca cgc atc aag gcc ggt atc	624
Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile	
195 200 205	
cag tcc gag gtc tat atg ggc aat ctg gat gcg gtc cgc gac tgg ggg	672
Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly	
210 215 220	
tac gcg ccc gaa tac gtc gaa ggc atg tgg cgg atg ctg cag acc gac	720
Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp	
225 230 235 240	

gag ccc gac c ttc gtt ttg gcg acc ggg cgc ggt tcc cc gtg cgt 768
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg
 245 250 255
 gag ttc gcg cgg gcc gcg ttc gag cat gcc ggt ttg gac tgg cag cag 816
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln
 260 265 270
 tac gtg aaa ttc gac caa cgc tat ctg cgg ccc acc gag gtg gat tcg 864
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 ctg atc ggc gac gcg acc aag gct gcc gaa ttg ctg ggc tgg agg gct 912
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala
 290 295 300
 tcg gtg cac act gac gag ttg gct cgg atc atg gtc gac gcg gac atg 960
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met
 305 310 315 320
 gcg gcg ctg gag tgc gaa ggc aag ccg tgg atc gac aag ccg atg atc 1008
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile
 325 330 335
 gcc ggc cgg aca tga 1023
 Ala Gly Arg Thr
 340

<210> 33
 <211> 340
 <212> PRT
 <213> Mycobacterium

<400> 33
 Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
 1 5 10 15
 Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile
 20 25 30
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu
 50 55 60
 Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp
 65 70 75 80
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu
 100 105 110
 Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala
 115 120 125
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu
 130 135 140

Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Ile Val Tyr Ser
 145 150 155 160
 Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile
 195 200 205
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly
 210 215 220
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp
 225 230 235 240
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg
 245 250 255
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln
 260 265 270
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala
 290 295 300
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met
 305 310 315 320
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile
 325 330 335
 Ala Gly Arg Thr
 340

<210> 34
 <211> 732
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(729)

<400> 34
 atg agg ctg gcc cgt cgc gct cgg aac atc ttg cgt cgc aac ggc atc 48
 Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile
 1 5 10 15
 gag gtg tcg cgc tac ttt gcc gaa ctg gac tgg gaa cgc aat ttc ttg 96
 Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu
 20 25 30

cgc caa ctc a tcg cat cgg gtc agt gcc gtg ctc gtc gcc ggg gcc	144
Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala	
35 40 45	
aat tcg ggg cag tac gcc agg ggt ctg cgc ggc gcg ggc ttc gcg ggc	192
Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly	
50 55 60	
cgc atc gtc tcg ttc gag ccg ctg ccc ggg ccc ttt gcc gtc ttg cag	240
Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln	
65 70 75 80	
cgc agc gcc tcc acg gac ccg ttg tgg gaa tgc cgg cgc tgt gcg ctg	288
Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu	
85 90 95	
ggc gat gtc gat gga acc atc tcg atc aac gtc gcc ggc aac gag ggc	336
Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly	
100 105 110	
gcc agc agt tcc gtc ttg ccg atg ttg aaa cga cat cag gac gcc ttt	384
Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe	
115 120 125	
cca cca gcc aac tac gtg ggc gcc caa cgg gtg ccg ata cat cga ctc	432
Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu	
130 135 140	
gat tcc gtg gct gca gac gtt ctg cgg ccc aac gat att gcg ttc ttg	480
Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu	
145 150 155 160	
aag atc gac gtt caa gga ttc gag aag cag gtg atc gcg ggt ggc gat	528
Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp	
165 170 175	
tca acg gtg cac gac cga tgc gtc ggc atg cag ctc gag ctg tct ttc	576
Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe	
180 185 190	
cag ccg ttg tac gag ggt ggc atg ctc atc cgc gag gcg ctc gat ctc	624
Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu	
195 200 205	
gtg gat tcg ttg ggc ttt acg ctc tcg gga ttg caa ccc ggt ttc acc	672
Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr	
210 215 220	
gac ccc cgc aac ggt cga atg ctg cag gcc gat ggc atc ttc ttc cgg	720
Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg	
225 230 235 240	
ggc agc gat tga	732
Gly Ser Asp	

<210> 35

<211> 243

<212> PRT

<213> Mycobacterium

<400> 35
 Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile
 1 5 10 15
 Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu
 20 25 30
 Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala
 35 40 45
 Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly
 50 55 60
 Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln
 65 70 75 80
 Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu
 85 90 95
 Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly
 100 105 110
 Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe
 115 120 125
 Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu
 130 135 140
 Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu
 145 150 155 160
 Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp
 165 170 175
 Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe
 180 185 190
 Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu
 195 200 205
 Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr
 210 215 220
 Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg
 225 230 235 240
 Gly Ser Asp

<210> 36
 <211> 732
 <212> DNA
 <213> Mycobacterium
 <220>
 <221> CDS
 <222> (1)..(729)

<400> 36
 gtg aaa tcg ttg aaa ctc gct cgt ttc atc gcg cgt agc gcc gcc ttc 48
 Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe
 1 5 10 15
 gag gtt tcg cgc cgc tat tct gag cga gac ctg aag cac cag ttt gtg 96
 Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val
 20 25 30
 aag caa ctc aaa tcg cgt cgg gta gat gtc gtt ttc gat gtc ggc gcc 144
 Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala
 35 40 45
 aac tca gga caa tac gcc gcc ggc ctc cgc cga gca gca tat aag ggc 192
 Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly
 50 55 60
 cgc att gtc tcg ttc gaa ccg cta tcc gga ccg ttt acg atc ttg gaa 240
 Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu
 65 70 75 80
 agc aaa gcg tca acg gat cca ctt tgg gat tgc cgg cag cat gcg ttg 288
 Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu
 85 90 95
 ggc gat tct gat gga acg gtt acg atc aat atc gca gga aac gcc ggt 336
 Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly
 100 105 110
 cag agc agt tcc gtc ttg ccc atg ctg aaa agt cat cag aac gct ttt 384
 Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe
 115 120 125
 ccc ccg gca aac tat gtc ggt acc caa gag gcg tcc ata cat cga ctt 432
 Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu
 130 135 140
 gat tcc gtg gcg cca gaa ttt cta ggc atg aac ggt gtc gct ttt ctc 480
 Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu
 145 150 155 160
 aag gtc gac gtt caa ggc ttt gaa aag cag gtg ctc gcc ggg ggc aaa 528
 Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys
 165 170 175
 tca acc ata gat gac cat tgc gtc ggc atg caa ctc gaa ctg tcc ttc 576
 Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe
 180 185 190
 ctg ccg ttg tac gaa ggt ggc atg ctc att cct gaa gcc ctc gat ctc 624
 Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu
 195 200 205
 gtg tat tcc ttg ggc ttc acg ttg acg gga ttg ctg cct tgt ttc att 672
 Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile
 210 215 220
 gat gca aat aat ggt cga atg ttg cag gcc gac ggc atc ttt ttc cgc 720
 Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg
 225 230 235 240

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gag gac ga
Glu Asp Asp

<210> 37
<211> 243
<212> PRT
<213> Mycobacterium

<400> 37
Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe
1 5 10 15
Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val
20 25 30
Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala
35 40 45
Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly
50 55 60
Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu
65 70 75 80
Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu
85 90 95
Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly
100 105 110
Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe
115 120 125
Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu
130 135 140
Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu
145 150 155 160
Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys
165 170 175
Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe
180 185 190
Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu
195 200 205
Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile
210 215 220
Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg
225 230 235 240
Glu Asp Asp

<210> 38
<211> 828

<212> DNA
<213> Mycobacterium

<220>
<221> CDS
<222> (1)..(825)

<400> 38
atg gtg cag acg aaa cga tac gcc ggc ttg acc gca gct aac aca aag 48
Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys
1 5 10 15

aaa gtc gcc atg gcc gca cca atg ttt tcg atc atc atc ccc acc ttg 96
Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu
20 25 30

aac gtg gct gcg gta ttg cct gcc tgc ctc gac agc atc gcc cgt cag 144
Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln
35 40 45

acc tgc ggt gac ttc gag ctg gta ctg gtc gac ggc ggc tcg acg gac 192
Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp
50 55 60

gaa acc ctc gac atc gcc aac att ttc gcc ccc aac ctc ggc gag cgg 240
Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg
65 70 75 80

ttg atc att cat cgc gac acc gac cag ggc gtc tac gac gcc atg aac 288
Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn
85 90 95

cgc ggc gtg gac ctg gcc acc gga acg tgg ttg ctc ttt ctg ggc gcg 336
Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala
100 105 110

gac gac agc ctg tac gag gct gac acc ctg gcg cgg gtg gcc gcc ttc 384
Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe
115 120 125

att ggc gaa cac gag ccc agc gat ctg gta tat ggc gac gtg atc atg 432
Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met
130 135 140

cgc tca acc aat ttc cgc tgg ggt ggc gcc ttc gac ctc gac cgt ctg 480
Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu
145 150 155 160

ttg ttc aag cgc aac atc tgc cat cag gcg atc ttc tac cgc cgc gga 528
Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly
165 170 175

ctc ttc ggc acc atc ggt ccc tac aac ctc cgc tac cgg gtc ctg gcc 576
Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala
180 185 190

gac tgg gac ttc aat att cgc tgc ttt tcc aac cca gcg ctc gtc acc 624
Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr
195 200 205

cgc tac atg cgt gtc gtt gca agc tac aac gaa tgc ggc ctc 672
 Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu
 210 215 220
 agc aat acg atc gtc gac aag gag ttt ttg aag cgg ctg ccg atg tcc 720
 Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser
 225 230 235 240
 acg aga ctc ggc ata agg ctg gtc ata gtt ctg gtg cgc agg tgg cca 768
 Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro
 245 250 255
 aag gtg atc agc agg gcc atg gta atg cgc acc gtc att tct tgg cgg 816
 Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg
 260 265 270
 cgc cga cgt tag 828
 Arg Arg Arg
 275

<210> 39
 <211> 275
 <212> PRT
 <213> Mycobacterium

<400> 39
 Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys
 1 5 10 15
 Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu
 20 25 30
 Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln
 35 40 45
 Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp
 50 55 60
 Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg
 65 70 75 80
 Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn
 85 90 95
 Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala
 100 105 110
 Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe
 115 120 125
 Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met
 130 135 140
 Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu
 145 150 155 160
 Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly
 165 170 175

Leu Phe Glu Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Ala Val Leu Ala
 180 185 190

Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr
 195 200 205

Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu
 210 215 220

Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser
 225 230 235 240

Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro
 245 250 255

Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg
 260 265 270

Arg Arg Arg
 275

<210> 40
 <211> 24
 <212> DNA
 <213> Mycobacterium

<400> 40
 gatgccgtga ggaggtaaaag ctgc

24

<210> 41
 <211> 24
 <212> DNA
 <213> Mycobacterium

<400> 41
 gatacggctc ttgaatcctg cacg

24

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